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<110> IMMUNEX CORPORATION  
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<120> ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR

<130> 3492-WO

<140> --to be assigned--

<141> 2004-11-04

<150> 60/518,166

<151> 2003-11-07

<160> 77

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Homo sapien

<220>

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Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys  
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Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser  
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Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser  
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Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu  
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Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn  
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Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg  
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Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly  
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675 680 685

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Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr  
725 730 735

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser  
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755 760 765

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly  
770 775 780

Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly  
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
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tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
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Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
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 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
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Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc aac agc      96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser
           20           25           30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc      144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
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Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser
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ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag      240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
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cct gaa gat ttt gca gtg tat tac tgt cag cag tat gat cac tca gca      288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
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Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
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cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct 288  
 Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 11  
 <211> 327  
 <212> DNA  
 <213> Artificial

&lt;220&gt;

&lt;223&gt; Light chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(327)

&lt;400&gt; 11

gat att gtg ctg acc cag tct cca gcc acc ctg tct ttg tct cca ggg	48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt aac agc aac	 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
 atc tat ggt aca tcc tac agg gcc act ggc atc cca gac agg ttc agt	 192
Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
 ggc agt ggg tct ggg aca gac ttc act ctc acc atc acc aga ctg gag	 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu	
65 70 75 80	
 cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cca	 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
 ccg tgg acg ttc ggc caa ggg aca cga ctg gag att aaa	 327
Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys	
100 105	

&lt;210&gt; 12

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 12

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn
20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 13  
<211> 327  
<212> DNA  
<213> Artificial

<220>  
<223> Light chain variable sequence

<220>  
<221> CDS  
<222> (1)..(327)

<400> 13  
gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg 48  
Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
  
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc 96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
20 25 30  
  
tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc 144  
Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45  
  
atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt 192  
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60  
  
ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag 240  
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80  
  
cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct 288  
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95  
  
ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa 327  
Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 14  
<211> 109

<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 14

Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 15  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 15

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 16  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
115

<210> 17  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 17  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95  
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110  
gtc tcc tca 345  
Val Ser Ser  
115

<210> 18  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 18

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 19  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1) .. (345)

<400> 19  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 20  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 20

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 21  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 21  
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 22  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 23  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 23  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

[illegible]

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<210> 24
<211> 115
<212> PRT
<213> Artificial
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<220>  
<223> Synthetic Construct

<400> 24

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210>	25
<211>	345
<212>	DNA
<213>	Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 25

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg	48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

&lt;210&gt; 26

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 26

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 27  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 27  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                                  105                                  110

gtc tcc tca 345  
 Val Ser Ser  
                   115

<210> 28  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1                                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
                   20                                  25                                  30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
                   50                                  55                                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                                  70                                  75                                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
                   85                                  90                                  95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                                  105                                  110

Val Ser Ser  
                   115

<210> 29  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 29

gag	gtt	cag	ttg	gtg	cag	tct	ggg	gga	ggc	ttg	gta	cat	cct	ggg	ggg	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Gly	
1				5					10					15		

tcc	ctg	aga	ctc	tcc	tgt	gca	ggc	tct	gga	ttc	acc	ttc	agt	aga	aat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn	
			20					25					30			

gct	atg	ttc	tgg	gtt	cgc	cag	gct	cca	gga	aaa	ggg	ctg	gag	tgg	gta	144
Ala	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

tca	ggg	att	ggg	act	ggg	ggg	gcc	aca	aac	tat	gca	gac	tcc	gtg	aag	192
Ser	Gly	Ile	Gly	Thr	Gly	Gly	Ala	Thr	Asn	Tyr	Ala	Asp	Ser	Val	Lys	
	50					55					60					

ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	gcc	aag	aac	tcc	ttg	tat	ctt	240
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	
65					70				75					80		

caa	atg	aac	agc	ctg	aga	gcc	gag	gac	atg	gct	gtg	tat	tac	tgt	gca	288
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala	
				85					90					95		

aga	ggg	agg	tac	tgg	ttc	ccg	tgg	tgg	ggc	cag	gga	acc	ctg	gtc	acc	336
Arg	Gly	Arg	Tyr	Trp	Phe	Pro	Trp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
			100					105					110			

gtc	tcc	tca														345
Val	Ser	Ser														
			115													

&lt;210&gt; 30

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 30

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Gly	
1				5					10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn	
			20					25					30			

Ala	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 31  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 31  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95  
aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

gtc tcc tca  
Val Ser Ser  
115

345

<210> 32  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 32

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 33  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1) .. (345)

<400> 33  
gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95  
aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110  
gtc tcc tca 345  
Val Ser Ser  
115

<210> 34  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 35

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 35

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

gtc tcc tca 345  
Val Ser Ser  
115

<210> 36  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 36

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 37  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 37

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg  
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 38  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 38

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 39  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 39  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95  
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110  
gtc tcc tca 345  
Val Ser Ser  
115

<210> 40  
<211> 115

<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 40

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 41  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 41  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
           35                                  40                                  45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
           50                                  55                                  60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
           65                                  70                                  75                                  80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr, Tyr Cys Ala  
                                   85                                  90                                  95

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                                  105                                  110

gtc tcc tca 345  
 Val Ser Ser  
           115

<210> 42  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
                   20                                  25                                  30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
           35                                  40                                  45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
           50                                  55                                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                                  70                                  75                                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                   85                                  90                                  95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 43  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 43  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 44  
 <211> 115  
 <212> PRT  
 <213> Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

&lt;210&gt; 45

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 45

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 46  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
115

<210> 47  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 47  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30  
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60  
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80  
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95  
aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110  
gtc tcc tca 345  
Val Ser Ser  
115

<210> 48  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

&lt;400&gt; 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 49  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

&lt;400&gt; 49

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> 50  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
Val Ser Ser	
115	

<210> 51  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 51  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 52  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 52

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 53  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 53  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg gcc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 54  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 55  
 <211> 345

<212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 55  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 56  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 56  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 57  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 57  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                     85                    90                    95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                     100                    105                    110

gtc tcc tca 345  
 Val Ser Ser  
             115

<210> 58  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                    5                    10                    15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
                     20                    25                    30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                     35                    40                    45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
                     50                    55                    60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                    70                    75                    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                     85                    90                    95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                     100                    105                    110

Val Ser Ser  
             115

<210> 59  
 <211> 345  
 <212> DNA  
 <213> Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 59

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

&lt;210&gt; 60

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 60

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 61  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 61  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                                  105                                  110

gtc tcc tca 345  
 Val Ser Ser  
           115

<210> 62  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 62

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
                   20                                  25                                  30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
           35                                  40                                  45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
           50                                  55                                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                                  70                                  75                                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                   85                                  90                                  95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                                  105                                  110

Val Ser Ser  
           115

<210> 63  
 <211> 109  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 27A1 light chain variable region

<400> 63

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 64  
 <211> 116  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 27A1 heavy chain variable region

<400> 64

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val  
 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
                   100                                  105                                  110

Thr Val Ser Ser  
                   115

<210> 65  
 <211> 107  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 5A1 light chain variable region

<400> 65

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
   1                                  5                                  10                                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
                   20                                  25                                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
                   35                                  40                                  45

Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
                   50                                  55                                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
   65                                  70                                  75                                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu  
                                   85                                  90                                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
                   100                                  105

<210> 66  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 5A1 heavy chain variable region

<400> 66

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
   1                                  5                                  10                                  15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe  
 20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr  
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 67  
 <211> 107  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp  
 20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe  
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
 100 105

<210> 68  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ser Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys  
 85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser  
 115

<210> 69  
 <211> 107  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 1B7 light chain variable region

<400> 69

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ile Ala Ser Ile Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe  
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
 100 105

<210> 70  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Primers

<220>  
 <221> misc\_feature  
 <222> (21)..(21)  
 <223> N is A or G

<220>  
 <221> misc\_feature  
 <222> (24)..(24)  
 <223> N is G or T

<400> 70  
 gtcgacgccg ccaccatgga nttnngggctg agctgg

36

<210> 71  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Primers

<400> 71  
 cttgaccagg cagcccaggg c

21

<210> 72  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 72  
atcaaacgta cggtggctgc accatctgtc ttcata

36

<210> 73  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 73  
gtttaaacgc ggccgcggat cctaacactc tcccctgttg aagctcttt

49

<210> 74  
<211> 99  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 74  
gtcgacgccg ccaccatgga aaccccagcg cagcttctct tcctcctgct actctggctc  
ccagataccg ctagcgaaat tgtgttgacg cagtctcca

60

99

<210> 75  
<211> 99  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 75  
tggagactgc gtcaacacaa tttcgctagc ggtatctggg agccagagta gcaggaggaa  
gagaagctgc gctgggggtt ccatggtggc ggcgtcgac

60

99

<210> 76  
<211> 57  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

&lt;400&gt; 76

atgggggtcaa cgcctatcct tggcctcctc ctggctgttc tccaaggagt cgctagc

57

&lt;210&gt; 77

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr  
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro  
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp  
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe  
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu  
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys  
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser  
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys  
325